

## SEQUENCE LISTING

<110> CABEZON SILIVA, Teresa Elisa Virginia  
 ELLIS, Jonathan H.  
 GERARD, Catherine Marie Ghislaine  
 HAMBLIN, Paul A.  
 PALMANTIER, Remi, M.  
 VINALS Y DE BASSOLS, Carlota

<120> Immunogenic Compositions

<130> B45311

<140> To Be Assigned

<150> PCT/EP03/06096

<151> 2003-06-06

<150> GB 0213365.0

<151> 2002-06-11

<150> GB 0300914.9

<151> 2003-01-15

<160> 52

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<211> 429

<212> DNA

<213> Streptococcus pneumoniae

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<211> 336

<212> DNA

<213> Streptococcus pneumoniae

<400> 16

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<211> 1674

<212> DNA

<213> Homo sapiens

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<210> 18

<211> 1947

<212> DNA

<213> Artificial Sequence

<220>

<223> Hybrid gene between St. pneum. C-LytA, P2 T helper epitope and human P501S.

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<211> 1662

<212> DNA

<213> Artificial Sequence

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<223> Codon optimised human P501S

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<223> Codon optimised human P501S

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cctggcgagc	gtggccgctc	tcccctgtgg	tgccggcgcc	acctgcctct	ctcactcggt	1140
ggccgtggtc	accgccagcg	ccgccctgac	cgggttcacc	ttctctgccc	tgcagattct	1200
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aggcgacacc	gggggcccct	ccagcgagga	cagcctcatg	acctccttcc	tgccctggccc	1320
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ccccctcct	gcgctgtgcg	gggccagcgc	tgcgcacgtg	agcgtgcgcg	tgggtggggg	1440
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cgactccgcc	ttctctctca	gccaggtggc	cccgtccctc	ttcatgggct	ctatcgtcca	1560
gctgtctcag	agcgtcaccg	cttaccatgt	gtccgctgct	ggactgggct	tgggtggctat	1620
ttatttcgcc	accaggtggg	tgttcgacaa	gagcgacctg	gccaaatact	ccgcctgact	1680
cgaggcag						1688

<210> 22

<211> 1688

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon optimised human P501S

<400> 22

gacggctagc	gccaccatgg	tgcagcggct	gtgggtgtcc	cggctgctgc	gccatagaaa	60
ggcccagttg	ctgctggtga	acctgctgac	tttcggactg	gaggtgtgcc	tggctgcccg	120
gatcacgtac	gtgccccccc	tgctgctgga	ggtgggcgtg	gaggagaagt	tcatgacaat	180
ggtgctgggc	atcggtcccc	tccctgggcct	cgtgtgtgtg	cccctcctcg	ggagtgcgtc	240
cgatcattgg	cggggccgct	acggccgcgc	cagaccgttc	atctgggccc	tgagcctggg	300
catcctgctc	tctctcttcc	tgatcccccg	ggccggctgg	ctggccggcc	tgctgtgtcc	360
cgacccccgc	cctctggagc	tggccctcct	gatcctgggc	gtgggcctgc	tggacttctg	420
cggccaggtg	tgtttcactc	ccctggaggc	tctgctctcc	gacctcttcc	gcgaccccga	480
ccactgtagg	caggcttaca	gcgtgtacgc	cttcatgac	agtctggggg	gatgcctggg	540
ctatctgctg	cccgtatcgc	actgggacac	cagcgccttg	gccccctacc	tggggactca	600
ggaggagtgc	ctgttcggcc	tgctcacctt	gatcttctcg	acgtgcgtcg	ccgccaccct	660
gctggtggcc	gaggaggcgg	ccctggggcc	caccgagccc	gccgagggcc	tgagcgctcc	720
cagcctgagc	ccccattgct	gcccgtgcag	ggctaggctc	gccttcagga	atctgggctc	780
tttctgcccc	cgctgtcatc	agctgtgctg	tgcgatgcct	cgcaccctgc	gccgcctggt	840
cgtcgctgag	ctctgttcc	ggatggccct	gatgacgttc	accctcttct	acaccgactt	900
cgtgggggag	ggcctgtacc	agggcgtgcc	cagggccgag	cccggcaccg	aggctaggcg	960
ccattacgac	gagggcgtca	ggatgggctc	tctgggcctc	ttcctgcagt	gcgccatcag	1020
tctggtgttc	tctctggtga	tggaccggct	ggtgcagcgc	ttcggcaccc	gggccgtgta	1080
cctcgccctc	gtggcggttc	tcccctgcgc	cgccggcgcg	acctgcctgt	ctcattctgt	1140
cggcgtgggt	accgccagcg	ccgccctgac	cggcttcacc	ttcagtgcgc	tccagattct	1200
gccctacacc	ctggcgcttc	tgtaccatcg	cgagaagcag	gtgttctctg	ccaagtaccg	1260



```

cggggacaca gggggagctt cctctgagga cagcctgatg accagcttct tgcccggccc 1320
caagccgggg gcccctttcc ccaacggcca tgtcggggcg ggcggcagcg gcctgctccc 1380
tcccccccc gcccgtgtcg gcgctagtgc ctgcgacgtg agcgtgcggg tgggtggtggg 1440
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cgactccgcc ttctgtctct cccaggtggc gccagcctg ttcattggga gtatcgtgca 1560
gctgagccag agcgtgaccg cctacatggt gagcgccgcc ggcctggggg tgggtggccat 1620
ctactttgcc acccaggtcg tgttcgacaa gagcgatctc gccaaagtata gcgcctgact 1680
cgaggcag                                     1688

```

<210> 23

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Hybrid gene between St. pneum. C-LytA, P2 T helper  
epitope and a small portion of the 5' end of human  
P501S

<400> 23

```

atggcggccg cttacgtaca ttccgacggc tcttatccaa aagacaagtt tgagaaaatc 60
aatggcactt ggtactactt tgacagttca ggctatatgc ttgcagaccg ctggaggaag 120
cacacagacg gcaactggta ctggttcgac aactcaggcg aaatggctac aggctggaag 180
aaaatcgctg ataagtggta ctatttcaac gaagaaggtg ccatgaagac aggctgggtc 240
aagtacaagg acacttggta ctacttagac gctaaagaag gcgccatgca atacatcaag 300
gctaactcta agttcattgg tatcactgaa ggcgtcatgg tatcaaatgc ctttatccag 360
tcagcggacg gaacaggctg gtactacctc aaaccagacg gaacactggc agacaggcca 420
gaaaagttca tgtac                                     435

```

<210> 24

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Hybrid gene between St. pneum. C-LytA, P2 T helper  
epitope and a small portion of the 5' end of human  
P501S - codon-optimised

<400> 24

```

atggccgccc cctacgtgca tagcgacggg agctacccca aggacaagtt cgagaagatc 60
aacgggacat ggtactactt cgactcctcc ggctacatgc tcgccgaccg ctggcggaag 120
cacaccgacg gcaactggta ctggttcgat aactcgggag agatggccac cggctggaag 180
aagatcgccg acaagtggta ctatttcaac gaggagggcg ccatgaagac cggctgggtg 240

aagtataagg acacctggta ctacctgac gccaaaggagg gcgccatgca gtatatcaag 300
gccaacagca agttcatcgg catcaccgag ggagtgatgg tcagcaacgc ctttatccag 360
agcgccgacg gcaccggatg gtactacttg aagccggacg gcaccctcgc ggatcgggcc 420
gagaagttca tgtac                                     435

```

<210> 25

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Hybrid gene between St. pneum. C-LytA, P2 T helper  
epitope and a small portion of the 5' end of human  
P501S - codon-optimised

<400> 25

```
atggccgccg cctacgtgca cagcgacggg tcctacccaa aggacaagtt cgagaagatc 60
aacggcacgt ggtactatct cgacagcagc ggctacatgc tcgccgatcg ctggcgcaag 120
cacaccgacg ggaactggta ctggttcgac aactctggcg agatggctac ggggtggaag 180
aagatcgccg acaagtggta ctacttcaac gaggagggcg ccatgaagac cgggtgggtg 240
aagtacaagg acacctggta ctacctggac gctaaggagg gcgccatgca gtacatcaag 300
gccaaactcga agttcatcgg gatcaccgag ggcgtgatgg tcagtaacgc ttatcatccag 360
agcgcgggacg gcacaggctg gtattacctg aagcccgatg gcaccctggc ggacagacct 420
gagaaattca tgtac                                     435
```

<210> 26

<211> 464

<212> DNA

<213> Artificial Sequence

<220>

<223> Hybrid gene between St. pneum. C-LytA, P2 T helper  
epitope and a small portion of the 5' end of human  
P501S - codon-optimised

<400> 26

```
gacggctagc gccaccatgg ccgccgccta cgtgcatagc gacgggagct accccaagga 60
caagttcgag aagatcaacg ggacatggta ctacttcgac tcctccggct acatgctcgc 120
cgaccgctgg cggaagcaca ccgacggcaa ctggtactgg ttcgataact cgggagagat 180
ggccaccggc tggagaaga tgcgcggaaa gtggtactat ttcaacgagg agggcgccat 240
gaagaccggc tgggtgaagt ataaggacac ctggtactac ctcgacgcca aggagggcgc 300
catgcagtat atcaaggcca acagcaagtt catcggcatc accgagggag tgatggtcag 360
caacgccttt atccagagcg ccgacggcac cggatggtag tacttgaagc cggacggcac 420
cctcgcggat cggcccgaga agttcatgta ctgactcgag gcag                                     464
```

<210> 27

<211> 652

<212> PRT

<213> Artificial Sequence

<220>

<223> Hybrid protein between St. pneum. C-LytA, P2 T  
helper epitope and amino acids 51-553 of human  
P501S

<400> 27

```
Met Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys
 1           5           10           15
Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly Tyr
      20           25           30
Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp
      35           40           45
Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp
      50           55           60
Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val
      65           70           75           80
Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met
      85           90           95
```

Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	Gly	Val		
			100					105					110				
Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly	Trp	Tyr		
		115					120					125					
Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Lys	Phe	Met		
	130					135					140						
Tyr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys	Val	Pro		
145					150					155						160	
Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	Gly	Arg	Arg		
			165						170					175			
Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser	Leu	Phe		
			180						185					190			
Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro	Asp	Pro		
		195					200					205					
Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	Leu	Leu	Asp		
	210					215					220						
Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu	Ser	Asp		
225					230					235					240		
Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val	Tyr	Ala		
			245						250					255			
Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro	Ala	Ile		
		260					265						270				
Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln	Glu	Glu		
		275					280					285					
Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val	Ala	Ala		
	290					295					300						
Thr	Leu	Leu	Val	Ala	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu	Pro	Ala			
305					310					315				320			
Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro	Cys	Arg		
			325						330					335			
Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	Leu	His		
		340						345					350				
Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	Val	Ala		
		355					360					365					
Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	Thr		
	370					375					380						
Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro		
385					390					395				400			
Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	Ser		
			405						410					415			
Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	Val		
			420					425					430				
Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr	Leu	Ala		
		435					440					445					
Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu	Ser	His		
	450					455					460						
Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	Phe	Thr	Phe		
465					470					475				480			
Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His	Arg		
			485						490					495			
Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	Ala		
		500						505					510				
Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro	Lys	Pro		
		515					520					525					
Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	Leu		
	530					535					540						

Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp	Val	Ser
545					550					555					560
Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	Gly
				565					570					575	
Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	Leu
			580					585					590		
Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln	Leu	Ser
		595					600					605			
Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly	Leu	Val
	610					615					620				
Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp	Leu	Ala
625					630					635					640
Lys	Tyr	Ser	Ala	Gly	His	His	His	His	His	His					
				645					650						

<210> 28

<211> 1959

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding the Hybrid protein between St. pneum.  
C-LytA, P2 T helper epitope and amino acids 51-553  
of human P501S

<400> 28

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aatggcactt	ggtactactt	tgacagttca	ggctatatgc	ttgcagaccg	ctggaggaag	120
cacacagacg	gcaactggta	ctggttcgac	aactcaggcg	aaatggctac	aggctggaag	180
aaaatcgctg	ataagtggta	ctatttcaac	gaagaagggtg	ccatgaagac	aggctgggtc	240
aagtacaagg	acacttggtg	ctacttagac	gctaaagaag	gcgccatgca	atacatcaag	300
gctaactcta	agttcattgg	tatcactgaa	ggcgctcatg	tatcaaattgc	ctttatccag	360
tcagcggacg	gaacaggctg	gtactacctc	aaaccagacg	gaacactggc	agacaggcca	420
gaaaagtcca	tgtacatggg	gctgggcatt	gggccagtgc	tgggcctggg	ctgtgtcccc	480
ctcctaggct	cagccagtga	ccactggcgt	ggacgctatg	gccgccgccg	gcccttcac	540
tgggcactgt	ccttgggcat	cctgctgagc	ctctttctca	tcccaagggc	cggctggcta	600
gcagggctgc	tgtgcccggg	tcccaggccc	ctggagctgg	caactgctcat	cctgggcgtg	660
gggctgctgg	acttctgtgg	ccagggtgtg	ttcactccac	tggaggccct	gctctctgac	720
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ccctacctgg	gcaccagga	ggagtgcctc	tttggcctgc	tcacctcat	cttctcacc	900
tgcgtagcag	ccacactgct	ggtggctgag	gaggcagcgc	tgggccccac	cgagccagca	960
gaagggctgt	cggccccctc	cttgtcgccc	caactgctgtc	catgccgggc	ccgcttggct	1020
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tcagccctgc	agatcctgcc	ctacacactg	gcctccctct	accaccggga	gaagcaggtg	1500
ttcctgcccc	aataccgagg	ggacactgga	ggtgctagca	gtgaggacag	cctgatgacc	1560
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gtacgtgtgg	tggtgggtga	gcccaccgag	gccaggggtg	ttccgggccg	gggcatctgc	1740
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```

atgggctcca ttgtccagct cagccagtct gtcactgcct atatggtgtc tgccgcaggc 1860
ctgggtctgg tcgccattta ctttgctaca caggtagtat ttgacaagag cgacttggcc 1920
aaatactcag cgggtggaca ccatcaccat caccattaa 1959

```

```

<210> 29
<211> 507
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Human P501S (amino acids 55-553) fused to 6
      histidine residues

```

```

<400> 29
Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro Leu
 1          5          10          15
Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg
 20          25          30
Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe Leu
 35          40          45
Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg
 50          55          60
Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp Phe
 65          70          75          80
Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp Leu
 85          90          95
Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala Phe
100          105          110
Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile Asp
115          120          125
Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu Cys
130          135          140
Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala Thr
145          150          155          160
Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu
165          170          175
Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala
180          185          190
Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln
195          200          205
Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala Glu
210          215          220
Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr Asp
225          230          235          240
Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly
245          250          255
Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser Leu
260          265          270
Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val Met
275          280          285
Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala Ser
290          295          300
Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His Ser
305          310          315          320
Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe Ser
325          330          335

```

Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His	Arg	Glu
			340					345					350		
Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	Ala	Ser
		355					360					365			
Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro	Lys	Pro	Gly
	370					375					380				
Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	Leu	Leu
385					390					395					400
Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp	Val	Ser	Val
				405				410						415	
Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	Gly	Arg
			420					425					430		
Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	Leu	Ser
		435					440					445			
Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln	Leu	Ser	Gln
	450					455					460				
Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly	Leu	Val	Ala
465					470					475					480
Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp	Leu	Ala	Lys
				485				490						495	
Tyr	Ser	Ala	Gly	Gly	His	His	His	His	His	His					
			500					505							

<210> 30  
 <211> 1524  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> DNA encoding Human P501S (amino acids 55-553)  
 fused to 6 histidine residues

<400> 30  
 atggtgctgg gcattggtcc agtgctgggc ctggtctgtg tcccgctcct aggctcagcc 60  
 agtgaccact ggcgtggacg ctatggccgc cgccggccct tcatctgggc actgtccttg 120  
 ggcacacctg tgagcctctt tctcatccca agggccggct ggctagcagg gctgctgtgc 180  
 ccgatccca ggcacctgga gctggcactg ctcacacctg gcgtggggct gctggacttc 240  
 tgtggccagg tgtgcttcac tccactggag gccctgctct ctgacctctt ccgggacccg 300  
 gaccactgtc gccaggccta ctctgtctat gccttcatga tcagtcttgg gggctgcctg 360  
 ggctacctcc tgccctgcat tgactgggac accagtggcc tggcccccta cctgggcacc 420  
 caggaggagt gcctctttgg cctgctcacc ctcactttcc tcacctgctg agcagccaca 480  
 ctgctgggtg ctgaggaggc agcgctgggc cccaccgagc cagcagaagg gctgtcggcc 540  
 cctctcttgt cgccccactg ctgtccatgc cgggcccgct tggctttccg gaacctgggc 600  
 gccctgcttc cccggctgca ccagctgtgc tgccgcatgc cccgcaccct gcgccggctc 660  
 ttcgtggctg agctgtgcag ctggatggca ctcacgacct tcacgctgtt ttacacggat 720  
 ttcgtgggctg aggggctgta ccaggcgctg cccagagctg agccggggac cgaggcccg 780  
 agacactatg atgaaggcgt tcggatgggc agcctggggc tgttccctgca gtgcgccatc 840  
 tccctggctc tctctctggc catggaccgg ctggtgcagc gattcggcac tcgagcagtc 900  
 tatttgccca gtgtggcagc tttccctgtg gctgccggct ccacatgcct gtcccacagt 960  
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 cgaggggaca ctggaggtgc tagcagtgag gacagcctga tgaccagctt cctgccaggc 1140  
 cctaagcctg gagctccctt ccctaattga cacgtgggtg ctggaggcag tggcctgctc 1200  
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ggtgagccca ccgaggccag ggtgggtccg ggccggggca tctgcctgga cctcgccatc 1320
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cagctcagcc agtctgtcac tgcctatatg gtgtctgccc caggcctggg tctggtcgcc 1440
atttactttg ctacacaggt agtatttgac aagagcgact tggccaaata ctcagcgggt 1500
ggacaccatc accatcacca ttaa                                     1524

```

<210> 31

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> Human P501S (amino acids 1-34 fused to 55-553)  
fused to 6 histidine residues

<400> 31

```

Met Ala Ala Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg
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Lys Ala Gln Leu Leu Val Asn Leu Thr Phe Gly Leu Glu Val
      20          25          30
Cys Leu Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp
      35          40          45
Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly
      50          55          60
Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr
      65          70          75          80
Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala
      85          90          95
Asp Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp
      100          105          110
Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala
      115          120          125
Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly
      130          135          140
Val Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp
      145          150          155          160
Tyr Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe
      165          170          175
Met Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val
      180          185          190
Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg
      195          200          205
Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu
      210          215          220
Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp
      225          230          235          240
Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu
      245          250          255
Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser

      260          265          270
Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr
      275          280          285
Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala
      290          295          300
Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu
      305          310          315          320

```

Glu	Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val	Ala	
				325					330					335		
Ala	Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu	Pro	
				340				345					350			
Ala	Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro	Cys	
		355					360					365				
Arg	Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	Leu	
	370					375					380					
His	Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	Val	
385					390					395					400	
Ala	Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	
				405					410					415		
Thr	Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	
			420					425					430			
Pro	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	
		435					440					445				
Ser	Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	
	450					455					460					
Val	Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr	Leu	
465					470					475					480	
Ala	Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu	Ser	
				485				490						495		
His	Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	Phe	Thr	
			500				505						510			
Phe	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His	
	515					520						525				
Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	
	530					535					540					
Ala	Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro	Lys	
545					550					555					560	
Pro	Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	
				565				570						575		
Leu	Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp	Val	
		580						585					590			
Ser	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	
		595					600					605				
Gly	Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	
	610					615					620					
Leu	Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln	Leu	
625					630					635					640	
Ser	Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly	Leu	
				645				650						655		
Val	Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp	Leu	
			660				665						670			
Ala	Lys	Tyr	Ser	Ala	Gly	Gly	His	His	His	His	His	His				
		675					680					685				

<210> 32

<211> 2058

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding Human P501S (amino acids 1-34 fused to 55-553) fused to 6 histidine residues



<400> 32

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tccgacggct cttatccaaa agacaagttt gagaaaatca atggcacttg gtactacttt 180
gacagttcag gctatatgct tgcagaccgc tggaggaagc acacagacgg caactgggtac 240
tggttcgaca actcaggcga aatggctaca ggctggaaga aaatcgctga taagtgggtac 300
tatttcaacg aagaagggtgc catgaagaca ggctgggtca agtacaagga cacttgggtac 360
tacttagacg ctaaagaagg cgccatgcaa tacatcaagg ctaactctaa gttcattggt 420
atcactgaag gcgtcatggt atcaaagtc tttatccagt cagcggacgg aacaggctgg 480
tactacctca aaccagacgg aacactggca gacaggccag aaaagttcat gtacatggtg 540
ctgggcattg gtccagtgcg gggcctggtc tgtgtcccgc tcctaggctc agccagtgcg 600
cactggcggtg gacgctatgg ccgcccggcg cccttcatct gggcactgtc cttgggcgac 660
ctgctgagcc tctttctcat cccaaggggc ggctggctag cagggtgctg gtgcccggat 720
cccaggcccc tggagctggc actgctcatc ctgggcgtgg ggctgctgga cttctgtggc 780
caggtgtgct tcaactccact ggaggccctg ctctctgacc tcttccggga cccggaccac 840
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ctcctgcctg ccattgactg ggacaccagt gccctggccc cctacctggg caccaggag 960
gagtgcctct ttggcctgct caccctcatc ttcctcacct gcgtagcagc cacactgctg 1020
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ttgtcgcccc actgctgtcc atgccggggc cgcttggtt tccggaacct gggcgccctg 1140
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gctgagctgt gcagctggat ggactcatg accttcacgc tgttttacac ggatttcgtg 1260
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tatgatgaag gcgttcggat gggcagcctg gggctgttcc tgcagtgcgc catctccctg 1380
gtcttctctc tggctcatgga ccggctgggt cagcgattcg gcaactcgagc agtctatttg 1440
gccagtgtgg cagctttccc tgtggctgcc ggtgccacat gcctgtccca cagtgtggcc 1500
gtggtgacag cttcagccgc cctcaccggg ttcaccttct cagccctgca gatcctgccc 1560
tacacactgg cctccctcta ccaccggag aagcaggtgt tcctgcccga ataccgagg 1620
gacactggag gtgctagcag tgaggacagc ctgatgacca gcttcctgcc aggccctaag 1680
cctggagctc cttccctaa tggacacgtg ggtgctggag gcagtggcct gctcccacct 1740
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cccaccgagg ccagggtggt tccggggccg ggcattctgc tggacctcgc catcctggat 1860
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agccagtctg tcaactgccta tatggtgtct gccgcaggcc tgggtctggt cgccatttac 1980
tttgctacac aggtagtatt tgacaagagc gacttgacca aatactcagc ggggtggacac 2040
catcaccatc accattaa 2058
```

<210> 33

<211> 671

<212> PRT

<213> Artificial Sequence

<220>

<223> St. pneum. C-LytA portion fused to P2 T helper  
epitope fused to Human P501S (amino acids 55-553)  
fused to 6 histidine residues downstream of yeast  
alphaprepro signal sequence

<400> 33

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Met Ala Ala Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala
 1             5             10             15
Ser Ser Ala Leu Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro
             20             25             30
Lys Asp Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser
             35             40             45
Ser Gly Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn
             50             55             60
```

Trp	Tyr	Trp	Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	65	70	75	80
Ile	Ala	Asp	Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr	85	90	95	
Gly	Trp	Val	Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu	100	105	110	
Gly	Ala	Met	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	115	120	125	
Glu	Gly	Val	Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	130	135	140	
Gly	Trp	Tyr	Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	145	150	155	
Lys	Phe	Met	Tyr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	165	170	175	
Cys	Val	Pro	Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	180	185	190	
Gly	Arg	Arg	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	195	200	205	
Ser	Leu	Phe	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	210	215	220	
Pro	Asp	Pro	Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	225	230	235	
Leu	Leu	Asp	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	245	250	255	
Leu	Ser	Asp	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	260	265	270	
Val	Tyr	Ala	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	275	280	285	
Pro	Ala	Ile	Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	290	295	300	
Gln	Glu	Glu	Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	305	310	315	
Val	Ala	Ala	Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	325	330	335	
Glu	Pro	Ala	Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	340	345	350	
Pro	Cys	Arg	Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	355	360	365	
Arg	Leu	His	Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	370	375	380	
Phe	Val	Ala	Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	385	390	395	
Phe	Tyr	Thr	Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	405	410	415	
Ala	Glu	Pro	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	420	425	430	
Met	Gly	Ser	Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	435	440	445	
Ser	Leu	Val	Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	450	455	460	
Tyr	Leu	Ala	Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	465	470	475	
Leu	Ser	His	Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	485	490	495	
Phe	Thr	Phe	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	500	505	510	
Tyr	His	Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr				

	515		520		525										
Gly	Gly	Ala	Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly
	530					535					540				
Pro	Lys	Pro	Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly
545					550					555					560
Ser	Gly	Leu	Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys
				565					570					575	
Asp	Val	Ser	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val
			580					585					590		
Val	Pro	Gly	Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala
	595						600					605			
Phe	Leu	Leu	Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val
	610					615					620				
Gln	Leu	Ser	Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu
625					630				635						640
Gly	Leu	Val	Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser
				645					650					655	
Asp	Leu	Ala	Lys	Tyr	Ser	Ala	Gly	Gly	His	His	His	His	His	His	
			660					665						670	

<210> 34

<211> 2477

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding St. pneum. C-LytA portion fused to P2  
T helper epitope fused to Human P501S (amino acids  
55-553) fused to 6 histidine residues downstream  
of yeast alphaprepro signal sequence

<400> 34

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aactgggtact	ggttcgacaa	ctcaggcgaa	atggctacag	gctggaagaa	aatcgctgat	180
aagtgggtact	atttcaacga	agaaggtgcc	atgaagacag	gctgggtcaa	gtacaaggac	240
acttgggtact	acttagacgc	taaagaaggc	gccatgcaat	acatcaaggc	taactctaag	300
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acaggctggt	actacctcaa	accagacgga	acactggcag	acaggccaga	aatggcggcc	420
agatttcctt	caatttttac	tgcagtttta	ttcgcagcat	cctccgcatt	agcggccgct	480
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ctgggcattg	gtccagtgtc	gggcctggtc	tgtgtcccgc	tcctaggctc	agccagtgc	1020
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caggtgtgct	tactccact	ggaggccctg	ctctctgacc	tcttccggga	cccggaccac	1260
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```

<210> 35

<211> 595

<212> PRT

<213> Artificial Sequence

<220>

<223> Human P501S (amino acids 55-553) fused to 6  
histidine residues downstream of yeast alphaprepro  
signal sequence

<400> 35

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Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln Ile
          20          25          30
Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe Asp
          35          40          45
Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu Phe
          50          55          60
Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val Ser
          65          70          75          80
Leu Glu Lys Arg Glu Ala Glu Ala Met Val Leu Gly Ile Gly Pro Val
          85          90          95
Leu Gly Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp
          100          105          110
Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu
          115          120          125
Gly Ile Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala
          130          135          140
Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile
          145          150          155          160
Leu Gly Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro
          165          170          175
Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg
          180          185          190

Gln Ala Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu
          195          200          205

```



<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding Human P501S (amino acids 55-553)  
fused to 6 histidine residues downstream of yeast  
alphaneprepro signal sequence

<400> 36

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atgagtttcc tcaattttac tgcagtttta ttcgcagcat cctccgcatt agctgctcca 60
gtcaacacta caacagaaga tgaaacggca caaattccgg ctgaagctgt catcggttac 120
tcagatttag aaggggattt cgatgttgct gttttgccat tttccaacag cacaataaac 180
gggttattgt ttataaatac tactattgcc agcattgctg cttaaagaaga aggggtatct 240
ctcgagaaaa gagaggctga agccatgggtg ctgggcattg gtccagtgtc gggcctggtc 300
tgtgtcccg ctcctaggctc agccagtgtg cactggcggtg gacgctatgg ccgccgccgg 360
cccttcattc gggcactgtc cttgggcattc ctgctgagcc tctttctcat cccaagggcc 420
ggctggctag cagggtgtgt gtgcccggat cccaggcccc tggagctggc actgctcatc 480
ctgggcgtgg ggctgctgga cttctgtggc caggtgtgtc tcaactccact ggaggccctg 540
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atgatcagtc ttgggggctg cctgggctac ctccctgctg ccattgactg ggacaccagt 660
gccctggccc cctacctggg caccaggag gagtgccctc ttggcctgtc caccctcatc 720
ttcctcacct gcgtagcagc cacactgtgt gtggctgagg aggcagcgtc gggccccacc 780
gagccagcag aagggctgtc ggccccctcc ttgtcgcccc actgctgtcc atgccggggc 840
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gctgagccgg gcaccgaggc ccggagacac tatgatgaag gcgttcggat gggcagcctg 1080
gggctgttcc tgcagtgcgc catctccctg gtcttctctc tggcatgga ccggctggtg 1140
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aagcaggtgt tcctgcccac ataccgaggg gacactggag gtgctagcag tgaggacagc 1380
ctgatgacca gcttcctgcc aggccctaag cctggagctc cttccctaag tggacacgtg 1440
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gatgtctccg tacgtgtggt ggtgggtgag cccaccgagg ccagggtggt tccgggccgg 1560
ggcatctgcc tggacctgcg catcctggat agtgcccttc tgcgtgtcca ggtggcccca 1620
tccctgttta tgggctccat tgtccagctc agccagtctg tcaactgccta tatggtgtct 1680
gccgcaggcc tgggtctggt cgccatttac tttgctacac aggtagtatt tgacaagagc 1740
gacttggcca aatactcagc ggttgagcac catcaccatc accattaa 1788
```

<210> 37

<211> 1955

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding codon-optimised Human P501S (amino  
acids 51-553) fused to St.pneum. C-LytA P2 helper  
epitope C-Lyta

<400> 37

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gcggccgcgc caccatggcc gccgcctacg tgcatagcga cgggagctac cccaaggaca 60
agttcgagaa gatcaacggg acatgggtact acttcgactc ctccggctac atgctcgccg 120
accgctggcg gaagcacacc gacggcaact ggtactggtt cgataactcg ggagagatgg 180
ccaccggctg gaagaagatc gcggacaagt ggtactatct caacgaggag ggcgccatga 240
agaccggctg ggtgaagtat aaggacacct ggtactacct cgacgccaa gagggcgcca 300
tgagtatatat caaggccaac agcaagttca tcggcatcac cgaggagtg atggtcagca 360
```

acgcctttat	ccagagcgcc	gacggcaccc	gatggtacta	cttgaagccg	gacggcaccc	420
tcgcggatcg	gcccagagaag	ttcatgtaca	tgggtgctggg	catcgggccc	gtcctggggc	480
tcgtgtgtgt	gcccctcctc	gggagtgcgt	ccgatcattg	gcggggccgc	tacggccgcc	540
gcagaccggt	catctggggc	ctgagcctgg	gcacccctgt	ctctctcttc	ctgatccccc	600
gggcccggctg	gctggccggc	ctgctgtgtc	ccgacccccg	ccctctggag	ctggccctcc	660
tgatcctggg	cgtgggcctg	ctggacttct	gcggccaggt	gtgtttcact	cccctggagg	720
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gtcgcatgcc	tcgcaccctg	cgccgcctgt	tcgtcgctga	gctctgttcc	tggatggccc	1140
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ccaggggcca	gcccggcacc	gaggctaggc	gccattacga	cgagggcgtc	aggatgggct	1260
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tgggtcagcg	cttcggcacc	cgggccgtgt	acctcgctc	tgtggcggt	ttccccgtcg	1380
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cgcccagcct	gttcatgggc	agtatcgtgc	agctgagcca	gagcgtgacc	gcctacatgg	1860
tgagcgccgc	cggcctgggg	ttggtggcca	tctactttgc	caccaggtc	gtgttcgaca	1920
agagcgatct	cgccaagtat	agcgcctgag	gatcc			1955

<210> 38

<211> 2045

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding codon-optimised Human P501S (amino acids 1-553)  
fused to St.pneum. C-Lyta P2 helper epitope C-Lyta

<400> 38

gcggccgcgc	caccatggcc	gccgcctacg	tgcatagcga	cgggagctac	cccaaggaca	60
agttcgagaa	gatcaacggg	acatggtact	acttcgactc	ctccggctac	atgctcgccg	120
accgctggcg	gaagcacacc	gacggcaact	ggtactggtt	cgataactcg	ggagagatgg	180
ccaccggctg	gaagaagatc	gcggacaagt	ggtactatct	caacgaggag	ggcgccatga	240
agaccggctg	ggtgaagtat	aaggacacct	ggtactacct	cgacgccaa	gagggcgcca	300
tgacgtatat	caaggccaac	agcaagtcca	tcggcatcac	cgagggagtg	atggtcagca	360
acgcctttat	ccagagcgcc	gacggcaccc	gatggtacta	cttgaagccg	gacggcaccc	420
tcgcggatcg	gcccagagatg	gtgcagcggc	tgtgggtgtc	ccggctgctg	cgccatagaa	480
aggcccagtt	gctgctgggtg	aacctgctga	ctttcggaact	ggagggtgtg	ctggctgccg	540
tgggtgctggg	catcgggccc	gtcctggggc	tcgtgtgtgt	gccccctcct	gggagtgcgt	600
ccgatcattg	gcggggccgc	tacggccgcc	gcagaccgtt	catctggggc	ctgagcctgg	660
gcatcctgct	ctctctcttc	ctgatccccc	gggcccggctg	gctggccggc	ctgctgtgtc	720
ccgacccccg	ccctctggag	ctggccctcc	tgatcctggg	cgtggggcctg	ctggacttct	780
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gggagccac	cgaggctagg	gtcgtgcctg	gccgggggat	ctgcctggac	ctggccatcc	1860
tcgactccgc	cttcctgtct	tcccaggtgg	cgcccagcct	gttcattggg	agtatcgtgc	1920
agctgagcca	gagcgtgacc	gcctacatgg	tgagcgccgc	cggcctgggg	ttggtggcca	1980
tctactttgc	caccaggtc	gtgttcgaca	agagcgatct	cgccaagtat	agcgccctgag	2040
gatcc						2045

<210> 39

<211> 2105

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding St.pneum. C-LytA P2 helper epitope  
C-LytA fused to Human P501S (amino acids 51-553)  
fused to Human P501S (amino acids 1-50) -  
Codon-optimised

<400> 39

gcggccgcgc	caccatggcc	gccgcctacg	tgcatagcga	cgggagctac	cccaaggaca	60
agttcgagaa	gatcaacggg	acatggtact	acttcgactc	ctccggctac	atgctcgccg	120
accgctggcg	gaagcacacc	gacggcaact	ggtactggtt	cgataactcg	ggagagatgg	180
ccaccggctg	gaagaagatc	gcggacaagt	ggtactatct	caacgaggag	ggcgccatga	240
agaccggctg	ggtgaagtat	aaggacacct	ggtactacct	cgacgccaa	gagggcgcca	300
tgcatgtat	caaggccaac	agcaagttca	tcggcatcac	cgagggagt	atggtcagca	360
acgcctttat	ccagagcgcc	gacggcaccg	gatggtacta	cttgaagccg	gacggcacc	420
tcgcggatcg	gcccagaga	ttcatgtaca	tggtgctggg	catcgcccc	gtcctggggc	480
tcgtgtgtgt	gcccctctc	gggagtgcgt	ccgatcattg	gcggggccgc	tacggccgcc	540
gcagaccgtt	catctggggc	ctgagcctgg	gcctcctgct	ctctctcttc	ctgatcccc	600
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tgatcctggg	cgtgggcctg	ctggacttct	gcggccagg	gtgtttcact	cccctggagg	720
ctctgctctc	cgacctcttc	cgcgaccccc	accactgtag	gcaggcttac	agcgtgtacg	780
ccttcattgat	cagtctgggg	ggatgcctgg	gctatctgct	gcccgcctac	gactgggaca	840
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acagcctgat	gaccagcttc	ttgcccggcc	ccaagccggg	ggcccccttc	cccaacggcc	1620
atgtcggggc	ggcgccgagc	ggcctgctcc	ctcccccccc	cgccctgtgc	ggcgctagt	1680



```

cctgcgacgt gagcgtgagg gtggtggtgg gggagcccac cgaggctagg gtcgtgcctg 1740
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gccatagaaa ggcccagttg ctgctggtga acctgctgac tttcggactg gaggtgtgcc 2040
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gatcc 2105

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<210> 40

<211> 2105

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding Human P501S (amino acids 1-50) fused  
to St.pneum. C-LytA P2 helper epitope C-Lyta fused  
to Human P501S (amino acids 51-553) -  
Codon-optimised

<400> 40

```

gcggccgcgc caccatggtg cagcggctgt ggggtgtccc gctgctgcgc catagaaagg 60
cccagttgct gctggtgaac ctgctgactt tcggactgga ggtgtgcctg gctgccggga 120
tcacgtacgt gccccccctg ctgctggagg tgggcgtgga ggagatggcc gccgcctacg 180
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ggtactggtt cgataactcg ggagagatgg ccaccggctg gaagaagatc gcggacaagt 360
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gatggtacta cttgaagccg gacggcacc ctcgggatcg gcccgagaag ttcattgtaca 600
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agctgagcca gagcgtgacc gcctacatgg tgagcgccgc cggcctgggg ttggtggcca 2040
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gatcc 2105

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<210> 41  
 <211> 652  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> St.pneum. C-LytA P2 helper epitope C-Lyta fused to  
 Human P501S

<400> 41  
 Met Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys  
 1 5 10 15  
 Phe Glu Lys Ile Asn Gly Thr Trp Tyr Phe Asp Ser Ser Gly Tyr  
 20 25 30  
 Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp  
 35 40 45  
 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp  
 50 55 60  
 Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val  
 65 70 75 80  
 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met  
 85 90 95  
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val  
 100 105 110  
 Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr  
 115 120 125  
 Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe Met  
 130 135 140  
 Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro  
 145 150 155 160  
 Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg  
 165 170 175  
 Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe  
 180 185 190  
 Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro  
 195 200 205  
 Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp  
 210 215 220  
 Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp  
 225 230 235 240  
 Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala  
 245 250 255  
 Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile  
 260 265 270  
 Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu  
 275 280 285  
 Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala  
 290 295 300  
 Thr Leu Leu Val Ala Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala  
 305 310 315 320  
 Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg  
 325 330 335  
 Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His  
 340 345 350  
 Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala  
 355 360 365

Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	Thr
370						375					380				
Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro
385					390					395					400
Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	Ser
				405					410					415	
Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	Val
			420					425					430		
Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr	Leu	Ala
	435						440					445			
Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu	Ser	His
450						455					460				
Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	Phe	Thr	Phe
465					470					475					480
Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His	Arg
				485					490					495	
Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	Ala
			500					505					510		
Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro	Lys	Pro
		515					520					525			
Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	Leu
	530					535					540				
Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp	Val	Ser
545					550					555					560
Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	Gly
				565					570					575	
Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	Leu
			580					585					590		
Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln	Leu	Ser
		595					600					605			
Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly	Leu	Val
	610					615					620				
Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp	Leu	Ala
625					630					635					640
Lys	Tyr	Ser	Ala	Gly	Gly	His	His	His	His	His	His				
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<210> 42

<211> 1959

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding St.pneum. C-LytA P2 helper epitope  
C-LytA fused to Human P501S (plus his tag)

<400> 42

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gctaactcta agttcattgg tatcactgaa ggcgtcattg tatcaaatgc ctttatccag 360
tcagcggacg gaacaggctg gtactacctc aaaccagacg gaacactggc agacaggcca 420
gaaaagttca tgtacatggt gctgggcatt ggtccagtgc tgggcctggt ctgtgtcccc 480

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atgggctcca ttgtccagct cagccagtct gtcactgcct atatggtgtc tgccgcaggc 1860
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<210> 43  
 <211> 553  
 <212> PRT  
 <213> Homo sapiens

<400> 43

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			20					25					30		
Ala	Ala	Gly	Ile	Thr	Tyr	Val	Pro	Pro	Leu	Leu	Leu	Glu	Val	Gly	Val
		35					40					45			
Glu	Glu	Lys	Phe	Met	Thr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly
	50					55					60				
Leu	Val	Cys	Val	Pro	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	
65					70				75					80	
Arg	Tyr	Gly	Arg	Arg	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile
			85					90						95	
Leu	Leu	Ser	Leu	Phe	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu
			100					105					110		
Leu	Cys	Pro	Asp	Pro	Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly
		115					120					125			
Val	Gly	Leu	Leu	Asp	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu
	130					135					140				
Ala	Leu	Leu	Ser	Asp	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala
145					150				155					160	
Tyr	Ser	Val	Tyr	Ala	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr
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Leu	Leu	Pro	Ala	Ile	Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu



<400> 44

Met	Ala	Ala	Ala	Tyr	Val	His	Ser	Asp	Gly	Ser	Tyr	Pro	Lys	Asp	Lys
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Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr	Phe	Asp	Ser	Ser	Gly	Tyr
			20					25					30		
Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn	Trp	Tyr	Trp
		35					40					45			
Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	Ile	Ala	Asp
	50					55					60				
Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr	Gly	Trp	Val
65					70				75					80	
Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu	Gly	Ala	Met
				85					90					95	
Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	Gly	Val
			100					105					110		
Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly	Trp	Tyr
		115					120					125			
Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Lys	Phe	Met
	130					135					140				
Tyr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys	Val	Pro
145					150					155					160
Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	Gly	Arg	Arg
				165					170					175	
Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser	Leu	Phe
			180					185					190		
Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro	Asp	Pro
		195					200					205			
Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	Leu	Leu	Asp
	210					215				220					
Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu	Ser	Asp
225					230				235					240	
Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val	Tyr	Ala
				245					250					255	
Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro	Ala	Ile
			260					265					270		
Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln	Glu	Glu
		275					280					285			
Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val	Ala	Ala
	290					295					300				
Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu	Pro	Ala
305					310					315					320
Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro	Cys	Arg
				325					330					335	
Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	Leu	His
			340					345					350		
Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	Val	Ala
		355					360					365			
Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	Thr
	370					375					380				
Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro
385					390				395						400
Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	Ser
				405					410					415	
Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	Val

			420					425					430				
Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr	Leu	Ala		
			435					440					445				
Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu	Ser	His		
			450				455					460					
Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	Phe	Thr	Phe		
465					470					475					480		
Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His	Arg		
			485						490					495			
Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	Ala		
			500					505					510				
Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro	Lys	Pro		
			515				520					525					
Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	Leu		
			530			535					540						
Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp	Val	Ser		
545					550				555					560			
Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	Gly		
			565					570						575			
Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	Leu		
			580					585					590				
Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln	Leu	Ser		
			595				600					605					
Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly	Leu	Val		
			610			615					620						
Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp	Leu	Ala		
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Lys	Tyr	Ser	Ala														

<210> 45

<211> 644

<212> PRT

<213> Artificial Sequence

<220>

<223> Codon-optimised hybrid protein between St.pneum. C-LytA P2 helper epitope C-Lyta fused to Human P501S amino acids 51-553)

<400> 45

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			20					25					30				
Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn	Trp	Tyr	Trp		
		35					40					45					
Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	Ile	Ala	Asp		
		50				55					60						
Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr	Gly	Trp	Val		
65					70				75						80		
Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu	Gly	Ala	Met		
			85					90						95			
Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	Gly	Val		
			100					105					110				
Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly	Trp	Tyr		

		115				120				125					
Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Lys	Phe	Met
	130					135					140				
Tyr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys	Val	Pro
145					150					155					160
Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	Gly	Arg	Arg
				165					170					175	
Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser	Leu	Phe
			180					185					190		
Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro	Asp	Pro
	195					200						205			
Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	Leu	Leu	Asp
	210					215					220				
Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu	Ser	Asp
225					230					235					240
Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val	Tyr	Ala
				245					250					255	
Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro	Ala	Ile
		260						265					270		
Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln	Glu	Glu
		275					280					285			
Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val	Ala	Ala
	290					295				300					
Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu	Pro	Ala
305					310					315					320
Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro	Cys	Arg
				325					330					335	
Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	Leu	His
			340					345					350		
Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	Val	Ala
		355					360					365			
Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	Thr
	370					375					380				
Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro
385					390					395					400
Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	Ser
				405					410					415	
Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	Val
			420					425					430		
Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr	Leu	Ala
	435						440					445			
Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu	Ser	His
	450					455					460				
Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	Phe	Thr	Phe
465					470					475					480
Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His	Arg
				485					490					495	
Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	Ala
		500						505					510		
Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro	Lys	Pro
		515					520					525			
Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	Leu
	530					535					540				
Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp	Val	Ser
545					550					555					560
Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	Gly



				565					570					575			
Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	Leu		
			580					585					590				
Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln	Leu	Ser		
		595					600					605					
Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly	Leu	Val		
	610					615					620						
Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp	Leu	Ala		
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Lys	Tyr	Ser	Ala														

<210> 46

<211> 694

<212> PRT

<213> Artificial Sequence

<220>

<223> St.pneum. C-LytA P2 helper epitope C-Lyta fused to  
Human P501S (amino acids 1-553)- codon optimised

<400> 46

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Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr	Phe	Asp	Ser	Ser	Gly	Tyr		
			20					25					30				
Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn	Trp	Tyr	Trp		
		35					40					45					
Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	Ile	Ala	Asp		
	50					55					60						
Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr	Gly	Trp	Val		
65					70				75						80		
Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu	Gly	Ala	Met		
			85						90					95			
Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	Gly	Val		
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Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly	Trp	Tyr		
		115					120					125					
Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Met	Val	Gln		
	130					135					140						
Arg	Leu	Trp	Val	Ser	Arg	Leu	Leu	Arg	His	Arg	Lys	Ala	Gln	Leu	Leu		
145					150					155					160		
Leu	Val	Asn	Leu	Leu	Thr	Phe	Gly	Leu	Glu	Val	Cys	Leu	Ala	Ala	Gly		
				165					170					175			
Ile	Thr	Tyr	Val	Pro	Pro	Leu	Leu	Leu	Glu	Val	Gly	Val	Glu	Glu	Lys		
			180						185				190				
Phe	Met	Thr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys		
		195					200					205					
Val	Pro	Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	Gly		
	210					215					220						
Arg	Arg	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser		
225					230					235					240		
Leu	Phe	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro		
				245					250					255			
Asp	Pro	Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	Leu		
			260					265					270				

Leu	Asp	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu		
		275					280					285					
Ser	Asp	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val		
	290				295						300						
Tyr	Ala	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro		
305					310					315					320		
Ala	Ile	Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln		
				325					330					335			
Glu	Glu	Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val		
			340					345				350					
Ala	Ala	Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu		
		355					360					365					
Pro	Ala	Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro		
	370					375					380						
Cys	Arg	Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg		
385					390					395					400		
Leu	His	Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe		
			405						410					415			
Val	Ala	Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe		
		420						425					430				
Tyr	Thr	Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala		
		435					440					445					
Glu	Pro	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met		
	450					455					460						
Gly	Ser	Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser		
465					470					475					480		
Leu	Val	Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr		
			485						490					495			
Leu	Ala	Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu		
			500					505					510				
Ser	His	Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	Phe		
		515					520					525					
Thr	Phe	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr		
	530					535					540						
His	Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly		
545					550					555					560		
Gly	Ala	Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro		
				565					570					575			
Lys	Pro	Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser		
			580					585					590				
Gly	Leu	Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp		
		595					600					605					
Val	Ser	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val		
	610					615					620						
Pro	Gly	Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe		
625					630					635					640		
Leu	Leu	Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln		
				645					650					655			
Leu	Ser	Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly		
			660					665					670				
Leu	Val	Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp		
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Leu	Ala	Lys	Tyr	Ser	Ala												
	690																

<211> 694

<212> PRT

<213> Artificial Sequence

<220>

<223> St.pneum. C-LytA P2 helper epitope C-Lyta fused to  
Human P501S (amino acids 51-553) fused to Human  
P501S (amino acids 1-50) - codon-optimised

<400> 47

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Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr	Phe	Asp	Ser	Ser	Gly	Tyr
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Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn	Trp	Tyr	Trp
		35					40					45			
Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	Ile	Ala	Asp
	50					55					60				
Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr	Gly	Trp	Val
65					70					75				80	
Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu	Gly	Ala	Met
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Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	Gly	Val
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Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly	Trp	Tyr
		115					120					125			
Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Lys	Phe	Met
	130					135					140				
Tyr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys	Val	Pro
145				150						155					160
Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	Gly	Arg	Arg
			165					170						175	
Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser	Leu	Phe
		180						185					190		
Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro	Asp	Pro
		195					200					205			
Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	Leu	Leu	Asp
	210					215					220				
Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu	Ser	Asp
225					230					235					240
Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val	Tyr	Ala
			245						250					255	
Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro	Ala	Ile
		260						265					270		
Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln	Glu	Glu
		275					280					285			
Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val	Ala	Ala
	290					295					300				
Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu	Pro	Ala
305					310					315					320
Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro	Cys	Arg
			325						330					335	
Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	Leu	His
			340					345					350		
Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	Val	Ala
	355						360					365			
Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	Thr



Gln	Leu	Leu	Leu	Val	Asn	Leu	Leu	Thr	Phe	Gly	Leu	Glu	Val	Cys	Leu	
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Ala	Ala	Gly	Ile	Thr	Tyr	Val	Pro	Pro	Leu	Leu	Leu	Glu	Val	Gly	Val	
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Glu	Glu	Met	Ala	Ala	Ala	Tyr	Val	His	Ser	Asp	Gly	Ser	Tyr	Pro	Lys	
	50					55					60					
Asp	Lys	Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr	Phe	Asp	Ser	Ser	
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Gly	Tyr	Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn	Trp	
			85					90						95		
Tyr	Trp	Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	Ile	
			100					105					110			
Ala	Asp	Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr	Gly	
		115					120					125				
Trp	Val	Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu	Gly	
	130					135					140					
Ala	Met	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	
145					150					155					160	
Gly	Val	Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly	
				165				170						175		
Trp	Tyr	Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Lys	
			180					185					190			
Phe	Met	Tyr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys	
		195					200					205				
Val	Pro	Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	Gly	
	210					215					220					
Arg	Arg	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser	
225					230					235					240	
Leu	Phe	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro	
				245				250						255		
Asp	Pro	Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	Leu	
			260					265					270			
Leu	Asp	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu	
		275					280					285				
Ser	Asp	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val	
	290					295					300					
Tyr	Ala	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro	
305					310					315					320	
Ala	Ile	Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln	
				325					330					335		
Glu	Glu	Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val	
			340					345					350			
Ala	Ala	Thr	Leu	Leu	Val	Ala	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu		
		355					360				365					
Pro	Ala	Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro	
	370					375					380					
Cys	Arg	Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	
385					390					395					400	
Leu	His	Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	
				405					410					415		
Val	Ala	Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	
			420					425					430			
Tyr	Thr	Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	
		435					440					445				
Glu	Pro	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	
	450					455					460					
Gly	Ser	Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	

465					470					475					480
Leu	Val	Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr
				485					490					495	
Leu	Ala	Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu
			500					505					510		
Ser	His	Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	Phe
		515					520					525			
Thr	Phe	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr
	530				535						540				
His	Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly
545				550						555				560	
Gly	Ala	Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro
				565					570					575	
Lys	Pro	Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser
			580					585					590		
Gly	Leu	Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp
		595					600					605			
Val	Ser	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val
	610					615					620				
Pro	Gly	Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe
625				630						635					640
Leu	Leu	Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln
			645					650					655		
Leu	Ser	Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly
		660					665					670			
Leu	Val	Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp
	675						680					685			
Leu	Ala	Lys	Tyr	Ser	Ala										
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<210> 49  
 <211> 1971  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> DNA encoding Human MUC-1 fused to St.pneum. C-LytA  
 P2 helper epitope C-LytA

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 cagagaagtt cagtgccag ctctactgag aagaatgctg tgagtatgac cagcagcgta 180  
 ctctccagcc acagcccggg ttcaggctcc tccaccactc agggacagga tgtcactctg 240  
 gccccggcca cggaaccagc ttcagggtca gctgccacct ggggacagga tgtcacctcg 300  
 gtcccagtc ccaggccagc cctgggctcc accaccccgc cagcccacga tgtcacctca 360  
 gccccggaca acaagccagc cccgggctcc accgcccccc cagcccacgg tgtcacctcg 420  
 gccccggaca ccaggccgccc cccgggctcc accgcccccc cagcccacgg tgtcacctcg 480  
 gccccggaca ccaggccgccc cccgggctcc accgcccccc cagcccacgg tgtcacctcg 540  
 gccccggaca ccaggccgccc cccgggctcc accgcccccc cagcccacgg tgtcacctcg 600  
 gccccggaca acaggccgccc cttggcgctcc accgcccccc cagtccacaa tgtcacctcg 660  
 gcctcagggt ctgcatcagg ctgagcttct actctgggtg acaacggcac ctctgccagg 720  
 gctaccacaa ccccagccag caagagcact ccattctcaa ttcccagcca ccactctgat 780  
 actcctacca cccttgccag ccatagcacc aagactgatg ccagtagcac tcaccatagc 840  
 acggtacctc ctctcacctc ctccaatcac agcattctc cccaggtgtc tactggggtc 900

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tctttctttt tcctgtcttt tcacatttca aacctccagt ttaattcctc tctggaagat 960
cccagcaccg actactacca agagctgcag agagacattt ctgaaatgtt tttgcagatt 1020
tataaacaag ggggttttct gggcctctcc aatattaagt tcaggccagg atctgtggtg 1080
gtacaattga ctctggcctt ccgagaaggt accatcaatg tccacgacgt ggagacacag 1140
ttcaatcagt ataaaacgga agcagcctct cgatataacc tgacgatctc agacgtcagc 1200
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tactttgaca gttcaggcta tatgcttgca gaccgtgga ggaagcacac agacggcaac 1680
tggtactggt tcgacaactc aggcgaaatg gctacaggct ggaagaaaat cgctgataag 1740
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tggtactact tagacgctaa agaaggcgcc atgcaataca tcaaggctaa ctctaagtgc 1860
attggtatca ctgaaggcgt catggtatca aatgccttta tccagtcagc ggacggaaca 1920
ggctggtact acctcaaacc agacggaaca ctggcagaca ggccagaatg a 1971

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<210> 50

<211> 656

<212> PRT

<213> Artificial Sequence

<220>

<223> Human MUC-1 fused to St.pneum. C-LytA P2 helper  
epitope C-Lyta

<400> 50

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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
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Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35          40          45
Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
 50          55          60
Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
 65          70          75          80
Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
 85          90          95
Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
 100          105          110
Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
 115          120          125
Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
 130          135          140
Arg Pro Pro Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
 145          150          155          160
Ala Pro Asp Thr Arg Pro Pro Pro Gly Ser Thr Ala Pro Ala Ala His
 165          170          175
Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
 180          185          190
Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Asn Arg Pro Ala Leu
 195          200          205
Ala Ser Thr Ala Pro Pro Val His Asn Val Thr Ser Ala Ser Gly Ser
 210          215          220

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Ala	Thr	Thr	Thr	Pro	Ala	Ser	Lys	Ser	Thr	Pro	Phe	Ser	Ile	Pro	Ser
				245					250					255	
His	His	Ser	Asp	Thr	Pro	Thr	Thr	Leu	Ala	Ser	His	Ser	Thr	Lys	Thr
			260					265					270		
Asp	Ala	Ser	Ser	Thr	His	His	Ser	Thr	Val	Pro	Pro	Leu	Thr	Ser	Ser
	275						280					285			
Asn	His	Ser	Thr	Ser	Pro	Gln	Leu	Ser	Thr	Gly	Val	Ser	Phe	Phe	Phe
	290					295					300				
Leu	Ser	Phe	His	Ile	Ser	Asn	Leu	Gln	Phe	Asn	Ser	Ser	Leu	Glu	Asp
305					310					315					320
Pro	Ser	Thr	Asp	Tyr	Gln	Glu	Leu	Gln	Arg	Asp	Ile	Ser	Glu	Met	
			325					330					335		
Phe	Leu	Gln	Ile	Tyr	Lys	Gln	Gly	Gly	Phe	Leu	Gly	Leu	Ser	Asn	Ile
			340					345					350		
Lys	Phe	Arg	Pro	Gly	Ser	Val	Val	Val	Gln	Leu	Thr	Leu	Ala	Phe	Arg
		355					360					365			
Glu	Gly	Thr	Ile	Asn	Val	His	Asp	Val	Glu	Thr	Gln	Phe	Asn	Gln	Tyr
	370					375					380				
Lys	Thr	Glu	Ala	Ala	Ser	Arg	Tyr	Asn	Leu	Thr	Ile	Ser	Asp	Val	Ser
385					390					395					400
Val	Ser	Asp	Val	Pro	Phe	Pro	Phe	Ser	Ala	Gln	Ser	Gly	Ala	Gly	Val
				405					410					415	
Pro	Gly	Trp	Gly	Ile	Ala	Leu	Leu	Val	Leu	Val	Cys	Val	Leu	Val	Ala
			420					425					430		
Leu	Ala	Ile	Val	Tyr	Leu	Ile	Ala	Leu	Ala	Val	Cys	Gln	Cys	Arg	Arg
		435					440					445			
Lys	Asn	Tyr	Gly	Gln	Leu	Asp	Ile	Phe	Pro	Ala	Arg	Asp	Thr	Tyr	His
	450					455					460				
Pro	Met	Ser	Glu	Tyr	Pro	Thr	Tyr	His	Thr	His	Gly	Arg	Tyr	Val	Pro
465					470					475					480
Pro	Ser	Ser	Thr	Asp	Arg	Ser	Pro	Tyr	Glu	Lys	Val	Ser	Ala	Gly	Asn
				485					490					495	
Gly	Gly	Ser	Ser	Leu	Ser	Tyr	Thr	Asn	Pro	Ala	Val	Ala	Ala	Thr	Ser
			500					505					510		
Ala	Asn	Leu	Met	Ala	Ala	Ala	Tyr	Val	His	Ser	Asp	Gly	Ser	Tyr	Pro
		515					520					525			
Lys	Asp	Lys	Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr	Phe	Asp	Ser
	530					535					540				
Ser	Gly	Tyr	Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn
545					550					555					560
Trp	Tyr	Trp	Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys
				565					570					575	
Ile	Ala	Asp	Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr
			580					585					590		
Gly	Trp	Val	Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu
		595					600					605			
Gly	Ala	Met	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr
	610					615					620				
Glu	Gly	Val	Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr
625					630					635					640
Gly	Trp	Tyr	Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu
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<211> 2037  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> DNA encoding St.pneum. C-LytA P2 helper epitope  
C-Lyta fused to Human MUC-1

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aaaatcaatg gcacttggtg ctactttgac agttcaggct atatgcttgc agaccgctgg 180  
aggaagcaca cagacggcaa ctggtactgg ttcgacaact caggcgaaat ggctacaggc 240  
tggaagaaaa tcgctgataa gtggtactat ttcaacgaag aaggtgccat gaagacaggc 300  
tggtcaagt acaaggacac ttggtactac ttagacgcta aagaaggcgc catgcaatac 360  
atcaaggcta actctaagtt cattggtatc actgaaggcg tcatggtatc aaatgccttt 420  
atccagtcag cggacggaac aggctggtac tacctcaaac cagacggaac actggcagac 480  
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cttacagttg ttacaggttc tggatcatga agctctaccc caggtggaga aaaggagact 600  
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agcagcgtac tctccagcca cagccccggt tcaggctcct ccaccactca gggacaggat 720  
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to Human MUC-1

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